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Sequence Listing was accepted.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Durreshwar Anjum
Timestamp: [year=2010; month=3; day=30; hr=14; min=53; sec=12; ms=838; ]
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Application No: 10587723   Version No: 1.0

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Output Set:

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Finished: 2010-03-23 14:30:33.533
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Total Errors: 0
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Actual SeqID Count: 212

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Input Set:

Output Set:

Started:	2010-03-23 14:30:29.458
Finished:	2010-03-23 14:30:33.533
Elapsed:	0 hr(s) 0 min(s) 4 sec(s) 75 ms
Total Warnings:	212
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Actual SeqID Count:	212

Error code   Error Description

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<110>   MILLER, JEFFREY C.
        ZHANG, LEI

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<130>   8325-0036.31

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<150>   60/542,780
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ggtccgcagg agcaagtgtt tgttgttgcc atgcaacaag aaaaggggggc ggaggcacca   180

cgccagtcgt cagctcgctc ctcgtatacg caacatcagt ccccgcccct ggtcccactc   240

ctgccggaag gcgaagatcc cgttaggcct ggacgtattc tcgcgacatt tgccggtcgc   300

ccggcttgca ctgcggcgtt tcccgcgcgg gctacctcag ttctcgggcg tacggcgcgg   360

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gcaaaaaaag gagatccacc tctaccaaac atttgttgtt cagctccagg acccacggga   180

acccaggaga caggccacac agatgctaaa actgcagaat ctgggtaatt tggaaagaaa   240

gggtcaagag accagggata ctgtgggaca ttggagtcta cagagtagtg ttcttttatc   300

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cccagctaga actgaactgg aacaacagat tcttgaacca ctgtttggag cacttggtgc      540

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attacaattc actggccgtc gttt                                            624


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ccctgtggag ccacacccta gggttggcca atctactccc aggagcaggg agggcaggag      180

ccagggctgg gcataaaagt cagggcagag ccatctattg cttacatttg cttctgacac      240

aactgtgttc actagcaacc tcaaacagac accatggtgc atctgactcc tgaggagaag      300

tctgccgtta ctgccctgtg gggcaaggtg aacgtggatg aagttggtgg tgaggccctg      360

ggcaggttgg tatcaaggtt acaagacagg tttaaggaga ccaatagaaa ctgggcatgt      420

ggagacagag aagactcttg ggtttctgat aggcactgac tctctctgcc tattggtcta      480

ttttcccacc cttaggctgc tggtggtcta cccttggacc cagaggttct ttgagtcctt      540

tgggggatctg tccactcctg atgctgttat gggcaaccct aaggtgaagg ctcatggcaa      600

gaaagtgctc ggtgccttta gtgatggcct ggctcacctg gacaacctca agggcacctt      660

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<223>  an amplification product derived from a mutated beta-globin gene

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gtttgaagtc caactcctaa gccagtgcca gaagagccaa ggacaggtac ggctgtcatc   180

acttagacct caccctgtgg agccacaccc tagggttggc caatctactc ccaggagcag   240

ggagggcagg agccagggct gggcataaaa gtcagggcag agccatctat tgcttacatt   300

tgcttctgac acaactgtgt tcactagcaa cctcaaacag acaccatggt gcatctgact   360

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<220>
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<223>   target sequences for the 5-10 ZFP/FokI fusion protein

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<223>   target sequences for the 5-8 ZFP/FokI fusion protein

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<220>
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<223> FokI cleavage half-domain

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                20   25   30

Ser Arg Ser Asp Asn Leu Ser Glu His Ile Arg Thr His Thr Gly Glu
        35   40   45

Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg Asn Ala
    50   55   60

His Arg Ile Asn His Thr Lys Ile His Thr Gly Ser Gln Lys Pro Phe
65   70   75   80

Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp Thr Leu Ser
                85   90   95

Glu His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile
                100   105   110

Cys Gly Arg Lys Phe Ala Ala Arg Ser Thr Arg Thr Thr His Thr Lys
            115   120   125

Ile His Leu Arg Gln Lys Asp Ala Ala Arg Gly Ser Gln Leu Val Lys
    130   135   140

Ser Glu Leu Glu Glu Lys Lys Ser Glu Leu Arg His Lys Leu Lys Tyr
145   150   155   160

Val Pro His Glu Tyr Ile Glu Leu Ile Glu Ile Ala Arg Asn Ser Thr
                165   170   175

Gln Asp Arg Ile Leu Glu Met Lys Val Met Glu Phe Phe Met Lys Val
        180   185   190

Tyr Gly Tyr Arg Gly Lys His Leu Gly Gly Ser Arg Lys Pro Asp Gly
        195   200   205

Ala Ile Tyr Thr Val Gly Ser Pro Ile Asp Tyr Gly Val Ile Val Asp
    210   215   220

Thr Lys Ala Tyr Ser Gly Gly Tyr Asn Leu Pro Ile Gly Gln Ala Asp
225   230   235   240

Glu Met Gln Arg Tyr Val Glu Glu Asn Gln Thr Arg Asn Lys His Ile
                245   250   255

Asn Pro Asn Glu Trp Trp Lys Val Tyr Pro Ser Ser Val Thr Glu Phe
            260   265   270

Lys Phe Leu Phe Val Ser Gly His Phe Lys Gly Asn Tyr Lys Ala Gln
        275   280   285

Leu Thr Arg Leu Asn His Ile Thr Asn Cys Asn Gly Ala Val Leu Ser
    290   295   300

Val Glu Glu Leu Leu Ile Gly Gly Glu Met Ile Lys Ala Gly Thr Leu
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Thr Leu Glu Glu Val Arg Arg Lys Phe Asn Asn Gly Glu Ile Asn Phe
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<212> PRT
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<220>
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<223> FokI cleavage half-domain

<400> 17

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1   5   10   15

Ala Met Ala Glu Arg Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe
            20   25   30

Ser Arg Ser Asp Ser Leu Ser Arg His Ile Arg Thr His Thr Gly Glu
        35   40   45

Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Asp Ser Ser
    50   55   60

Asn Arg Lys Thr His Thr Lys Ile His Thr Gly Gly Gly Gly Ser Gln
65   70   75   80

Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp
                85   90   95

Ser Leu Ser Val His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala
            100   105   110

Cys Asp Ile Cys Gly Arg Lys Phe Ala Asp Arg Ser Asn Arg Ile Thr
        115   120   125

His Thr Lys Ile His Leu Arg Gln Lys Asp Ala Ala Arg Gly Ser Gln
    130   135   140

Leu Val Lys Ser Glu Leu Glu Glu Lys Lys Ser Glu Leu Arg His Lys
145   150   155   160

Leu Lys Tyr Val Pro His Glu Tyr Ile Glu Leu Ile Glu Ile Ala Arg
                165   170   175

Asn Ser Thr Gln Asp Arg Ile Leu Glu Met Lys Val Met Glu Phe Phe
            180   185   190

Met Lys Val Tyr Gly Tyr Arg Gly Lys His Leu Gly Gly Ser Arg Lys
        195   200   205

Pro Asp Gly Ala Ile Tyr Thr Val Gly Ser Pro Ile Asp Tyr Gly Val
    210   215   220

Ile Val Asp Thr Lys Ala Tyr Ser Gly Gly Tyr Asn Leu Pro Ile Gly
225   230   235   240

Gln Ala Asp Glu Met Gln Arg Tyr Val Glu Glu Asn Gln Thr Arg Asn
                245   250   255

Lys His Ile Asn Pro Asn Glu Trp Trp Lys Val Tyr Pro Ser Ser Val
        260   265   270

Thr Glu Phe Lys Phe Leu Phe Val Ser Gly His Phe Lys Gly Asn Tyr
        275   280   285

Lys Ala Gln Leu Thr Arg Leu Asn His Ile Thr Asn Cys Asn Gly Ala
    290   295   300

Val Leu Ser Val Glu Glu Leu Leu Ile Gly Gly Glu Met Ile Lys Ala
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Gly Thr Leu Thr Leu Glu Glu Val Arg Arg Lys Phe Asn Asn Gly Glu
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Ile Asn Phe

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ttcttcaagt ccgccatgcc cgaaggctac gtccaggagc gcaccatctt cttcaaggac      360

gacggcaact acaagacccg cgccgaggtg aagttcgagg gcgacaccct ggtgaaccgc      420

atcgagctga agggcatcga cttcaaggag gacggcaaca tcctgggggca caagctggag      480

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cagcagaaca ccccatcgg cgacggcccc gtgctgctgc ccgacaacca ctacctgagc      660

acccagtccg ccctgagcaa agaccccaac gagaagcgcg atcacatggt cctgctggag      720

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accctgaagt tcatctgcac caccggcaag ctgcccgtgc cctggcccac cctcgtgacc      240

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cttcaagtcc gccatgcccg aaggctacgt ccaggagcgc accatcttct tcaaggacga      360

cggcaactac aagacccgcg ccgaggtgaa gttcgagggc gacaccctgg tgaaccgcat      420

cgagctgaag ggcatcgact tcaaggagga cggcaacatc ctggggcaca agctggagta      480

caactacaac agccacaacg tctatatcat ggccgacaag cagaagaacg gcatcaaggt      540

gaacttcaag atccgccaca acatcgagga cggcagcgtg cagctcgccg accactacca      600

gcagaacacc cccatcggcg acggccccgt gctgctgccc gacaaccact acctgagcac      660

ccagtccgcc ctgagcaaag accccaacga gaagcgcgat cacatggtcc tgctggagtt      720

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ctgaagttca tctgcaccac cggcaagctg cccgtgccct ggcccaccct cgtgaccacc   180

ctgacctacg gcgtgcagtg cttcagccgc taccccgacc acatgaagca gcacgacttc   240

ttcaagtccg ccatgcccga aggctacgtc caggagcgca ccatcttctt caaggacgac   300

ggcaactaca gacccgcgc cgaggtgaag ttcgagggcg acaccctggt gaaccgcatc   360

gagctgaagg gcatcgactt caaggaggac ggcaacatcc tggggcacaa gctggagtac   420

aactacaaca gccacaacgt ctatatcatg gccgacaagc agaagaacgg catcaaggtg   480

aacttcaaga tccgccacaa catcgaggac ggcagcgtgc agctcgccga ccactaccag   540

cagaacaccc ccatcggcga cggccccgtg ctgctgcccg acaaccacta cctgagcacc   600

cagtccgccc tgagcaaaga ccccaacgag aagcgcgatc acatggtcct gctggagttc   660

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ctgaagttca tctgcaccac cggcaagctg cccgtgccct ggcccaccct cgtgaccacc   180

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gagctgaagg gcatcgactt caaggaggac ggcaacatcc tggggcacaa gctggagtac    420

aactacaaca gccacaacgt ctatatcatg gccgacaagc agaagaacgg catcaaggtg    480

aacttcaaga tccgccacaa catcgaggac ggcagcgtgc agctcgccga ccactaccag    540

cagaacaccc ccatcggcga cggccccgtg ctgctgcccg acaaccacta cctgagcacc    600

cagtccgccc tgagcaaaga ccccaacgag aagcgcgatc acatggtcct gctggagttc    660

gtgaccgccg ccgggatcac tctcggcatg gacgagctgt acaagtaaag cggccgctcg    720

agtctagagg gcccgtttaa acccgctgat cagcctcgac tgtgccttct agttgccagc    780

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